FiGURE 1

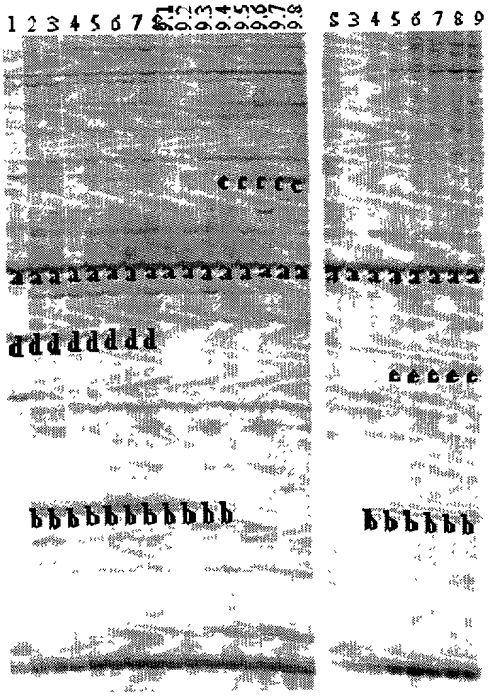

Figure 1. Differential display of loblolly pine zygotic and somatic embryos at different stages of development. The zygotic embryos (left panel) used were from tree BC-1 and the somatic embryos (right panel) are of genotype 260. Primer pair T12VC-AP3 (GenHunter, Nashville, TN) were used in the PCR reactions. The numbers on the top of the lanes indicate the stages of the embryos used. The letters superimposed on the images mark different types of banding patterns: (a), the band appeared in both embryos at all the stages; (b), early to middle stages in ZE and middle to late stages in SE; (c), late stages in ZE and absent in SE; (d), early stages in ZE and absent in SE; (e), present in SE but not in ZE.

FIGURE 2

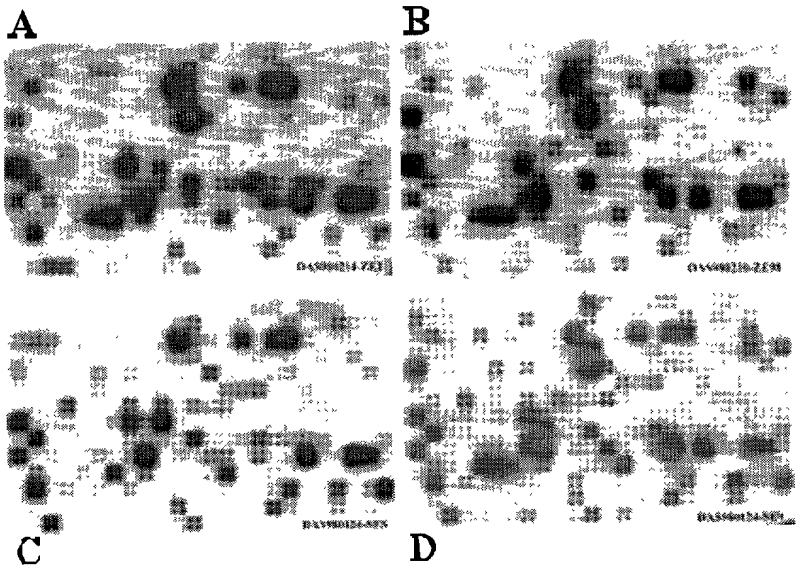

Figure 2. Detection of gene expression by high-density array Southern hybridization. Cloned cDNAs (327) were blotted on a membrane as high-density arrays. Each cDNA was blotted four times as a quadrate. The membranes were hybridized to the total cDNAs derived from total mRNA isolated from zygotic embryos at stage 1 (A), stage 9.8 (B), somatic embryos at suspension stage (C), and stage 9 (D). Dark spots indicate high level of gene expression and light spots indicate low level of gene expression.

FIGURE 3

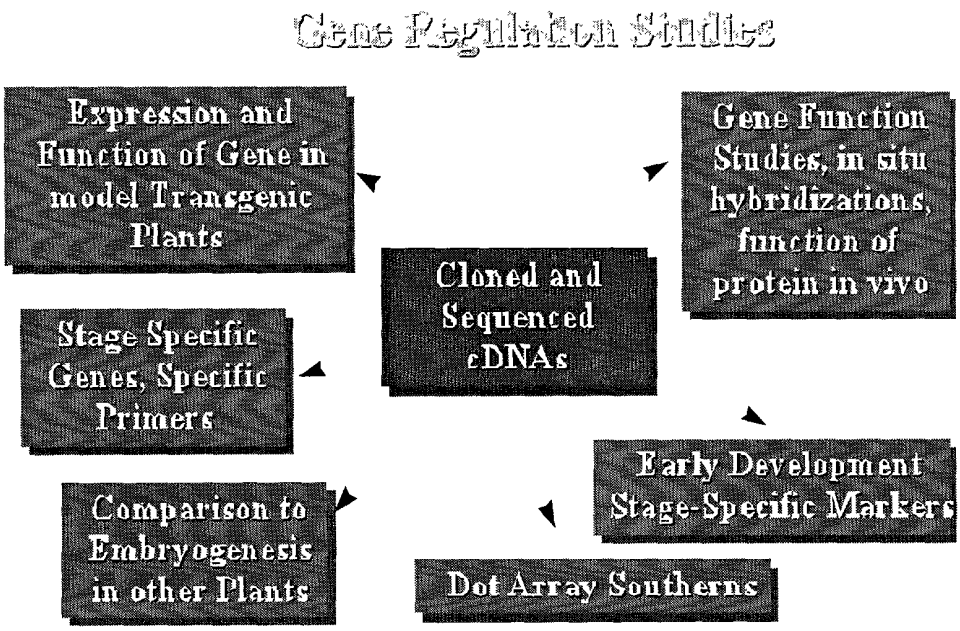

Figure 3. Gene regulation studies arising from the cDNA cloning of genes expressed in embryos. See text for their applicability to process improvement.